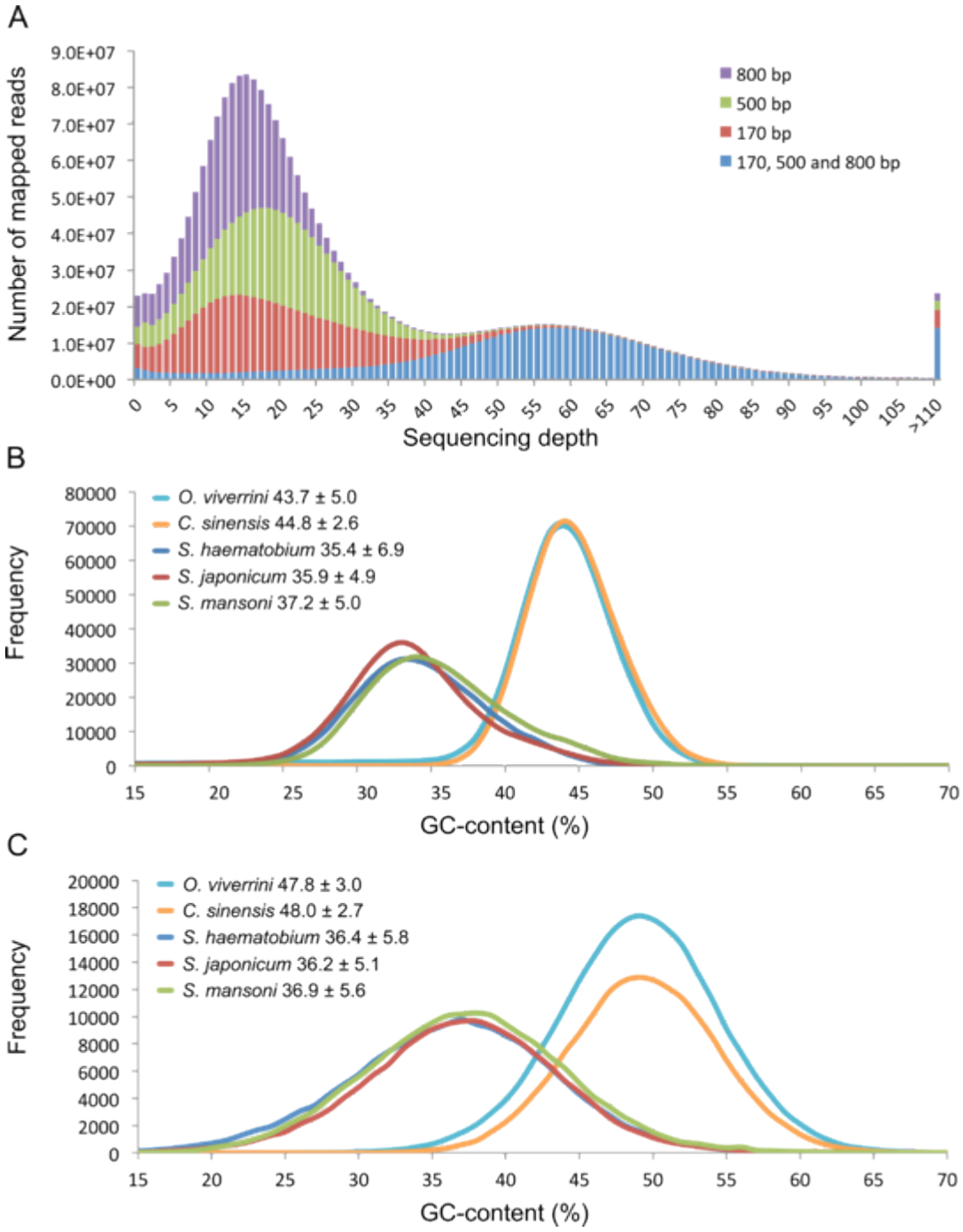
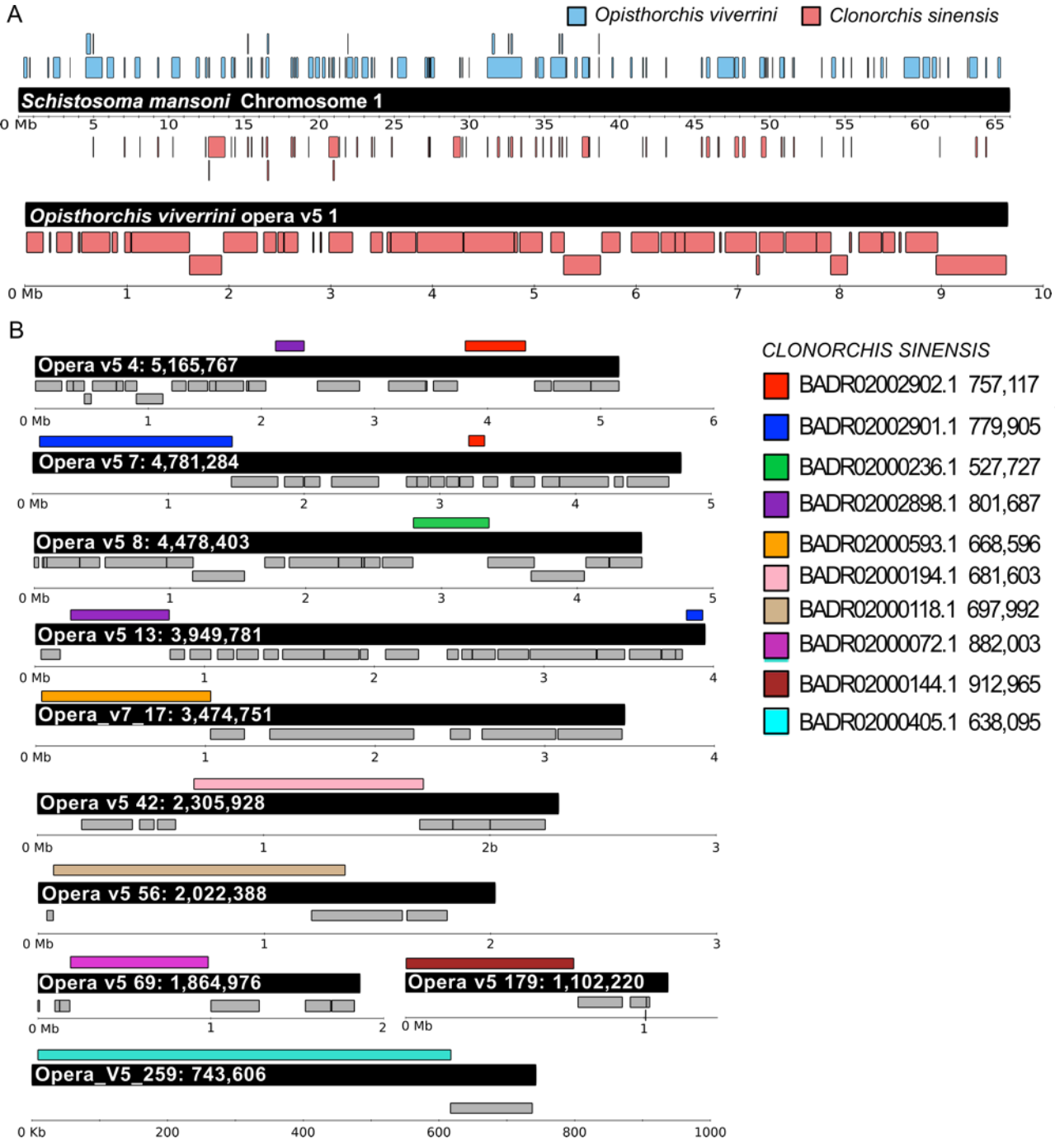
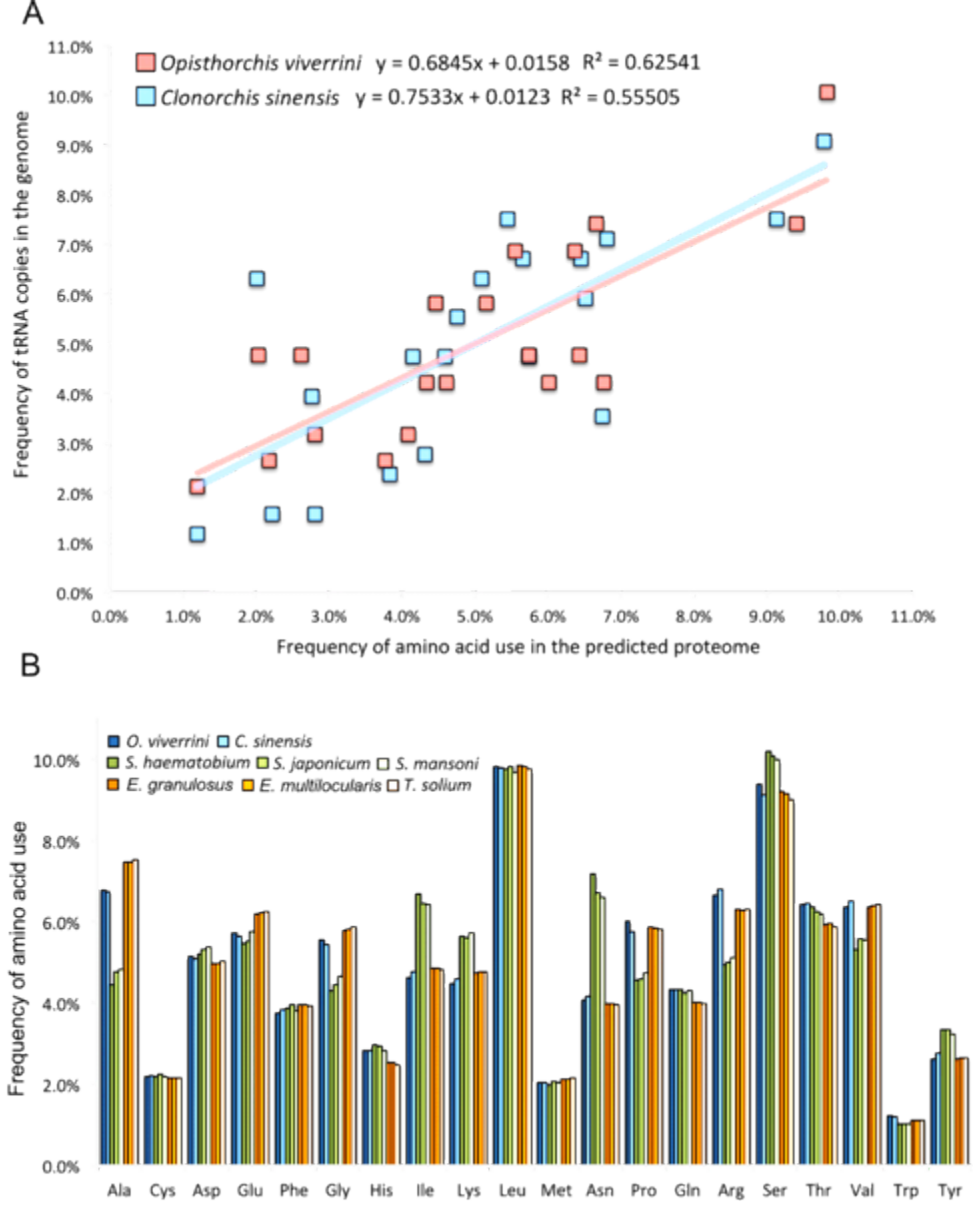


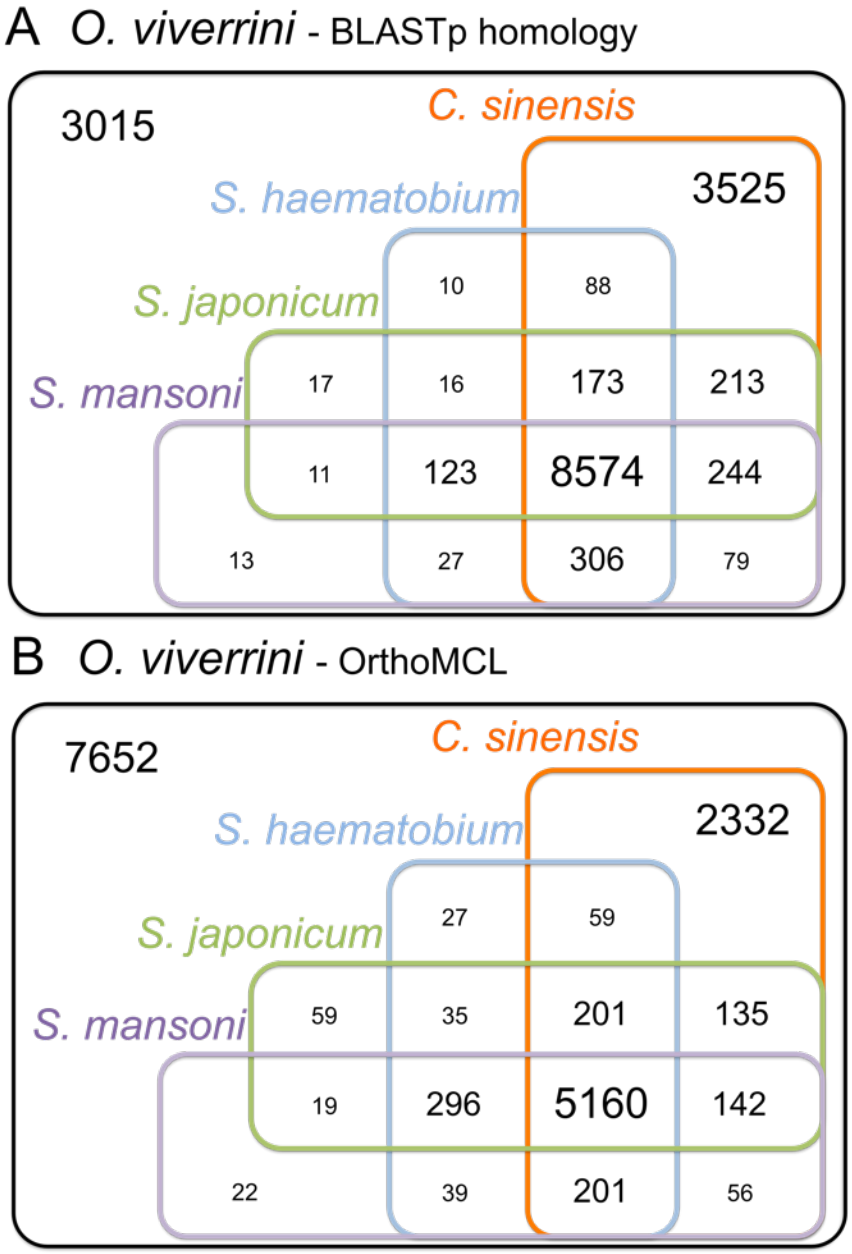
Supplementary Figure 1. Sequencing depth (A) and nucleotide composition of the *Opisthorchis viverrini* genome (B) and coding domains (C). A. A *k*-mer (17-base pair) frequency analysis of *O. viverrini* genomic sequence data produced from the 170 bp, 500 bp, 800 bp or 170, 500 + 800 bp insert libraries highlighting the read depth and coverage homogeneity for genomic DNA libraries used for genome assembly. B. The GC content of trematode genomes. The GC content of *O. viverrini, Clonorchis sinensis, Schistosoma haematobium*, *S. mansoni* and *S. japonicum* in 10 kilobase, non-overlapping sliding windows across their genomes. The *x*-axis indicates GC content, and the y-axis shows the sequencing depth frequency. C. The GC content of predicted coding domains encoded in trematode genomes. The GC content of *O. viverrini, C. sinensis, S. haematobium*, *S. mansoni* and *S. japonicum* in 100 bp, non-overlapping sliding windows across their coding domains. The *x*-axis indicates GC content, and the y-axis shows the sequencing depth frequency.



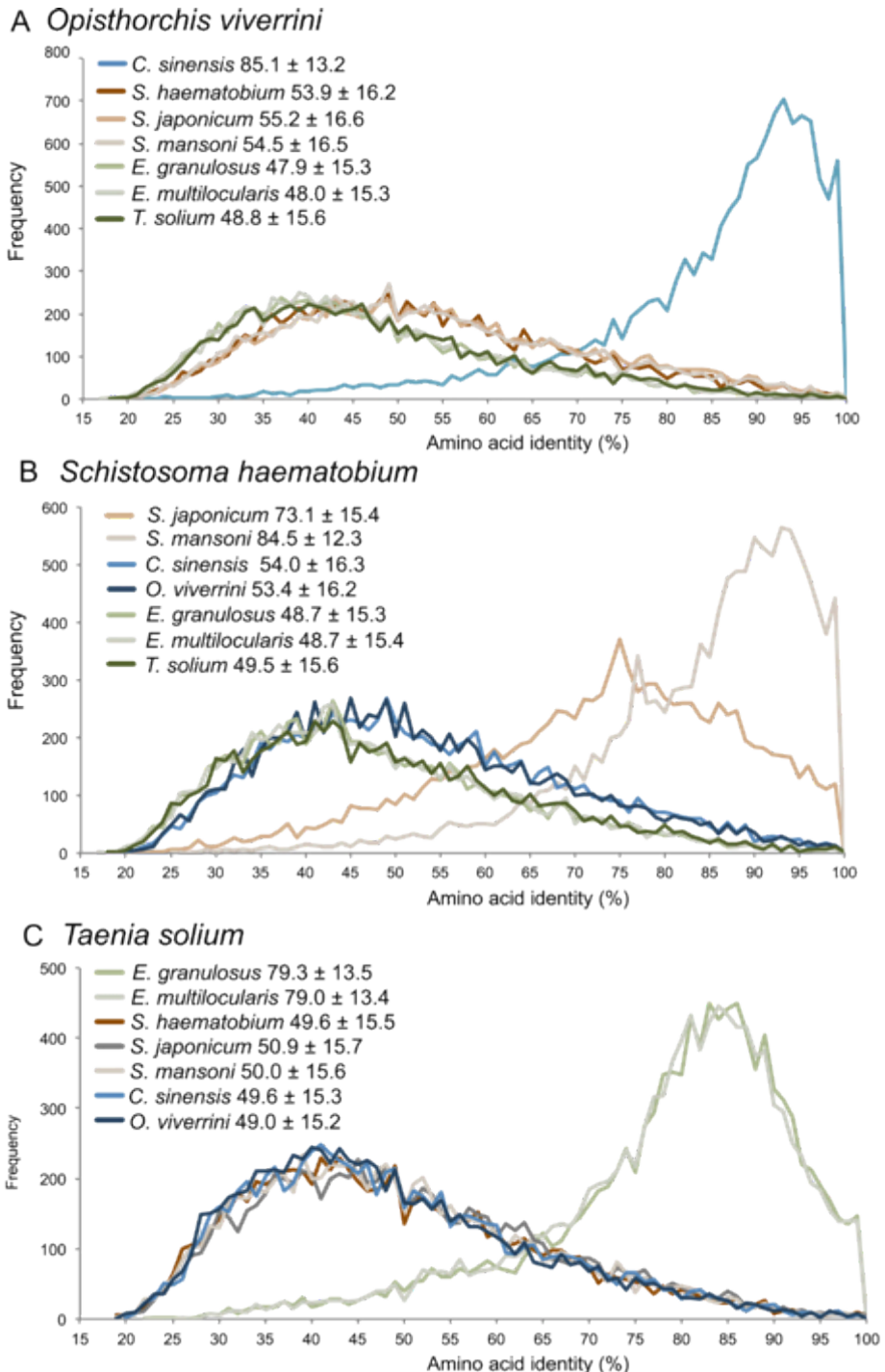
Supplementary Figure 2. Examples of the genome-wide comparisons of *Opisthorchis viverrini*, *Clonorchis sinensis* and *Schistosoma mansoni*. A. *O. viverrini* and *C. sinensis* genomic scaffolds (> 100 kilobases in length) inferred to be syntenic with *S. mansoni* chromosome 1 (65,476,000 bases in length) and *C. sinensis* genomic scaffolds (> 100 kb) inferred to be syntenic with the largest *O. viverrini* genome scaffold of *O. viverrini* (scaffold 1: 9,657,000 bases). B. Top 10 homologous scaffolds of *O. viverrini* and *C. sinensis*. Syntenic elements characterized among the top 10 scaffolds of each species are coloured according to *C. sinensis* genome scaffolds. The remaining syntenic blocks observed between the ten *O. viverrini* scaffolds and *C. sinensis* genome scaffolds (> 100 kb) are shown in grey.



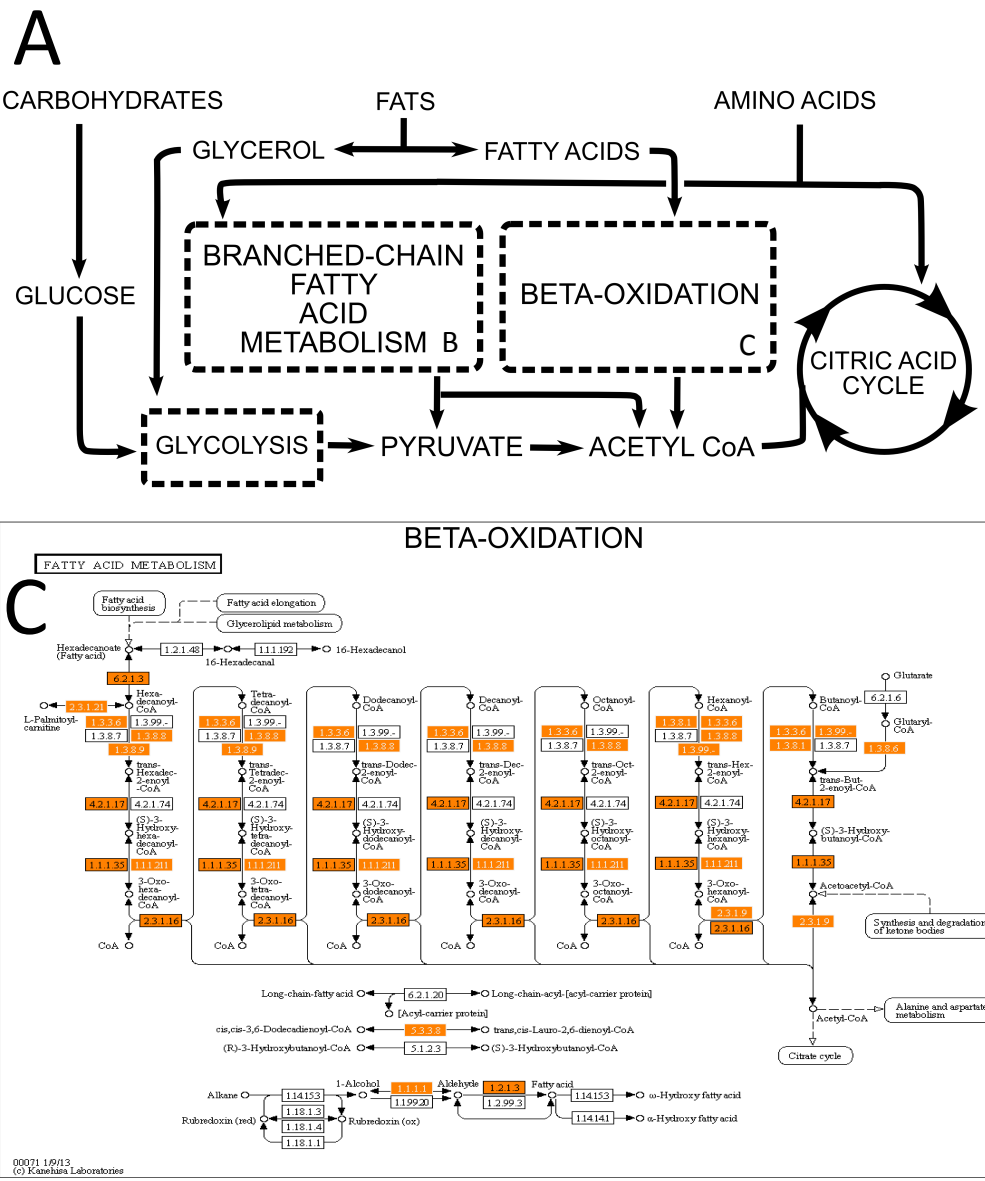
Supplementary Figure 3. A. Correlation between the frequency of transfer RNA (tRNA) copies and predicted use of amino acid residues in the *Opisthorchis viverrini* and *Clonorchis sinensis* genomes. B. Evidence of amino acid usage in the genomes of flatworms. Amino acid residue frequency within the predicted proteomes of opisthorchiid (*Clonorchis sinensis* and *Opisthorchis viverrini*) and schistosomatid (*Schistosoma haematobium*, *S. japonicum* and *S. mansoni*) flukes and tapeworms (*Echinococcus granulosus*, *E. multilocularis* and *Taenia solium*).

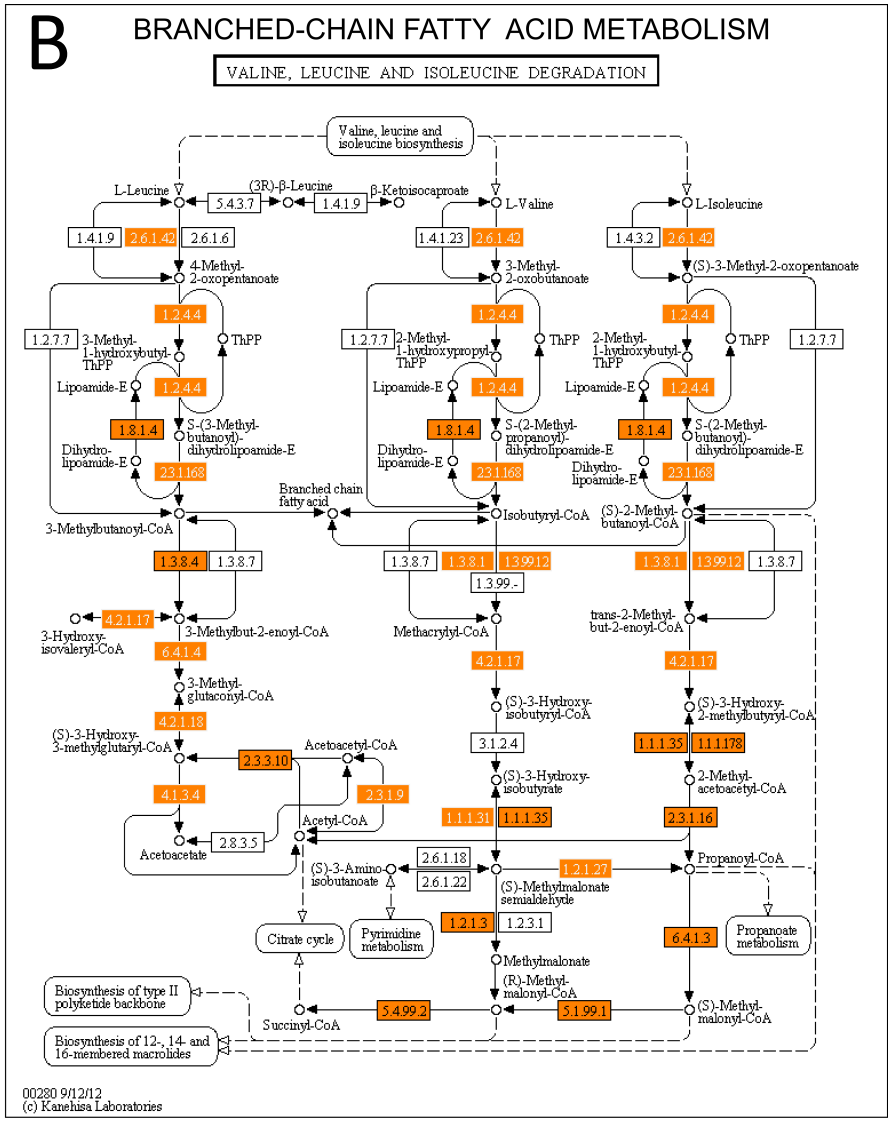


Supplementary Figure 4. Similarity of *Opisthorchis viverrini* (Opisthorchiidae) proteins to other trematodes for which predicted proteomes are available, including *Clonorchis sinensis* (Opisthorchiidae) and the blood flukes (Schistosomatidae), *Schistosoma haematobium*, *S. japonicum* and *S. mansoni*. Homology of proteins among the predicted proteomes based on homology (BLASTp, E-value < $1e^{-05}$) alone (A), and proteins clustered using OrthoMCL (B).

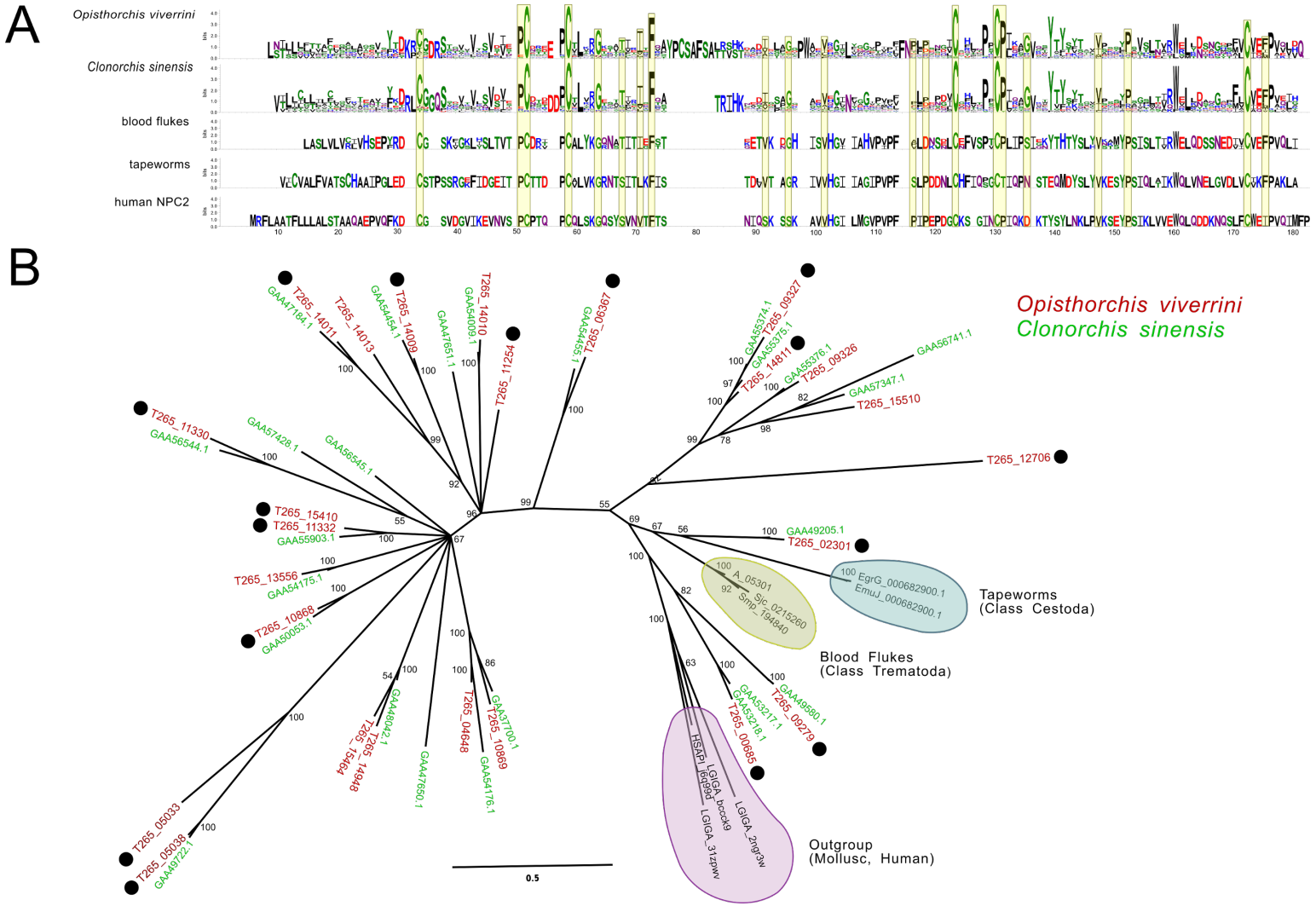


Supplementary Figure 5. Amino acid sequence homology (BLASTn, E-value ≤10-5) among representatives of parasitic flatworms affecting humans, including members of the families Opisthorchiidae (*Clonorchis sinensis* and *Opisthorchis viverrini*; Class Trematoda), Schistosomatidae (*Schistosoma haematobium*, *S. japonicum* and *S. mansoni*; Class Trematoda) and Taeniidae (*Echinoccus granulosus*, *E. multilocularis* and *Taenia solium*; Class Cestoda). Pairwise amino acid sequence homology of proteins predicted from the genomes of each parasitic flatworm, and compared relative to proteins predicted from *O. viverrini* (A), *S. haematobium* (B) and *T. solium* (C).





Supplementary Figure 6. A. Major catabolic pathways proposed for *Opisthorchis viverrini* metabolism living in the human bile duct. B. Conserved branched-chain amino acid degradation pathway conserved in opisthorchiid liver flukes. C. Conserved fatty acid catabolism pathway conserved in opisthorchiid liver flukes. Enzymes (see **Supplementary Table 15**) labeled in orange were found in *O. viverrini*, and those with white font were unique or otherwise different in opisthorchiid flukes *(including Clonorchis sinensis* and *O. viverrini*), when compared to select parasitic flatworms, including *Schistosoma haematobium*, *S. japonicum* and *S. mansoni* (Schistosomatidae; Class Trematoda) and *Echinococcus granulosus*, *E. multilocularis* and *Taenia solium* (Taeniidae; Class Cestoda) using OrthoMCL.



Supplementary Figure 7. *Opisthorchis viverrini* genes encoding proteins predicted to contain a novel MD-2-related lipid-recognition domain (Interproscan ID: IPR003172) and sharing amino acid sequence homology to human Niemann-Pick 2 protein (NPC2). A. Amino acid logos of frequently encoded aligned amino acid residues among 24 *O. viverrini*, 24 *Clonorchis sinensis,* 3 blood fluke (one each for *Schistosoma haematobium, S. japonicum* and *S. mansoni*) and 2 tapeworm (one each for *Echinococcus granulosus* and *E. multilocularis*) proteins. Logo is coloured based on amino acid chemistry, where amino acid residues are grouped by colour depending on their chemical characteristics, so that polar residues (G, S, T, Y & C) are green, neutral (Q & N) are purple, basic (K, R & H) are blue, acidic (D & E) are red and hydrophobic (A, V, L, I, P, W, F & M) are black. Conserved domains are highlighted in yellow. Residue height denotes the measure of uncertainty for each residue (in bits/symbol). B. Phylogenetic relationships of NPC2-like proteins among selected parasitic trematodes and cestodes. Values indicated on the branches represent Bayesian inference bootstrap support. *O. viverrini* and *C. sinensis* sequences are labeled in red and green respectively. O. viverrini proteins with transcriptional evidence of their expression in stages established in the bile duct are denoted with a black circle. For comparative purposes, tapeworms (Class Cestoda) are represented by *E. granulosus* and *E. multilocularis* and blood flukes are represented by *S. haematobium* (A_05301), *S. japonicum* (Sjc_0215260) and *S. mansoni* (Smp_194840). Gene sequences from a gastropod snail, *Lottia gigantea* (LGIGA) and human (HSAP) were included as an outgroup.

Supplementary Table 1. Genomic and transcriptomic sequence libraries constructed from *Opisthorchis viverrini*

Summary of the genomic DNA libraries, constructed from *O. viverrini*, and the features of the sequence data produced for subsequent genome assembly and annotation.

Descriptions		Insert size	Read length	Raw data (Gb)	Clean data (Gb)	Total clean sequence reads	Sequence reads mapped	% reads mapped	Predicted sequence coverage[a]	Correctly orientated pairs	% mapped reads correctly orientated
Genomic DNA											
Short insert libraries											
SZAXPI001112-4	Small insert/paired-end	170	100	18.50	16.13	171,551,320	154,646,840	90.15	24.37	72,681,123	84.73
OPIrlkD1ATDIAAPE	Small insert/paired-end	500	100	17.77	13.76	145,444,634	131,407,005	90.35	20.71	61,038,821	83.93
SZAXPI001123-5	Small insert/paired-end	800	100	13.38	10.64	116,962,352	103,399,286	88.40	16.30	45,908,822	78.50
Mate-paired libraries											
OPIqqsDAADWAAPEI-37	Large insert/mate paired-end	2000	100	23.70	18.21	371,691,618	282,764,259	76.07	44.57	42,290,340	22.76
OPIqqsDABDLAAPEI-13	Large insert/mate paired-end	5000	49	19.82	12.63	257,716,562	215,219,398	83.51	16.62	16,795,290	13.03
OPIheoDAGDTAAPEI-20	Large insert/mate paired-end	10000	49	19.29	7.74	157,877,824	134,485,097	85.18	10.39	14,899,346	18.87
OPIesmDFHDUAAPEI-95	Large insert/mate paired-end	20000	49	12.67	0.77	15,864,690	13,684,392	86.26	1.06	765,910	9.66
Total					79.88	1,237,109,000	1,035,606,277	83.7	134	254,379,652	41.12

Summary of the complementary (cDNA) constructed from *O. viverrini*, and the features of the sequence data produced for subsequent gene prediction and annotation.

		Insert size	Read length	Raw data (Gb)	Clean data (Gb)	Total clean sequence reads	RNA-seq reads mapped to genome (%)	RNA-seq reads mapped to coding domains (%)	Number of coding domains[b] supported with RNA-seq data
Complementary DNA of reverse transcribed messenger RNA									
Juvenile Illumina	Small insert/single-end	500	76	1.73	1.59	20,927,408	17,237,328 (82.37)	12,161,793 (58.11)	13,122 (80.87)
Adult Illumina	Small insert/single-end	500	76	1.24	0.84	11,095,483	9,546,563 (86.04)	6,341,127 (57.15)	13,247 (80.61)
Adult Roche 454	Small insert/single-end	500	373	0.24	0.23	606,603	591,883 (97.57)	432,042 (71.22)	12,058 (73.61)
Total					2.66	32,629,494	24,811,533 (76.04)	18,971,653 (58.14)	14,269 (87.11)

[a] Assuming equal sequencing of the genome, and based on a predicted genome size of 634,465,514 (see **Supplementary Table 2**).

[b] Based on a predicted gene set of 16,379 coding domains (see **Supplementary Table 3**).

Supplementary Table 2. Salient features of the *Opisthorchis viverrini* genome assessed during the genome assembly process.

	de novo assembly (SOAPdenovo)	Opera scaffolding (Opera)	Error correction (iCORN)	Scaffolds with annotation
Number of scaffolds:	158,119	149,573	149,573	1,719
Total size of scaffolds	619,811,986	634,459,549	634,465,514	592,395,591
Total number of Ns in genome	44,714,906	48,336,258	48,336,147	45,232,821
Longest scaffold	1,075,674	9,657,388	9,657,489	9,657,388
Shortest scaffold	100	100	100	200
Number of scaffolds > 1K nt	11,146	4,919	4,919	1,275
Number of scaffolds > 10K nt	4,822	1,136	1,136	870
Number of scaffolds > 100K nt	1,927	685	685	677
Number of scaffolds > 1M nt	3	201	201	201
Mean scaffold size	3,920	4,242	4,242	344,616
Median scaffold size	144	140	140	12,028
N50 scaffold length	191,538	1,323,917	1,323,951	1,396,068
Scaffold %A	26.1	26.0	26.0	26.0
Scaffold %C	20.3	20.2	20.2	20.2
Scaffold %G	20.3	20.2	20.2	20.2
Scaffold %T	26.1	26.0	26.0	26.0
Scaffold %N	7.2	7.6	7.6	7.6
Number of contigs	202,031	177,137	177,136	28,006
Number of contigs in scaffolds	50,095	29,289	29,287	27,200
Number of contigs not in scaffolds	151,936	147,848	147,849	806
Total size of contigs	575,152,844	586,152,758	586,158,758	547,190,608
Longest contig	196,428	338,609	338,609	338,609
Shortest contig	31	31	31	31
Number of contigs > 1K nt	48,865	29,746	29,747	25,634
Number of contigs > 10K nt	17,712	14,419	14,419	14,295
Number of contigs > 100K nt	56	526	526	526
Mean contig size	2,847	3,309	3,309	19,538
Median contig size	179	157	157	10,428
N50 contig length	19,046	37,268	37,267	40,390
Percentage of assembly in scaffolded contigs	92.70%	94.50%	94.50%	99.80%
Average number of contigs per scaffold	1.3	1.2	1.2	16.3
Average length of break (>25 Ns) between contigs in scaffold	1017	1752	1752	1719
Assessment of scaffold sequence iCORN correction using the number of mismatches observed between the *O. viverrini* genome and available *O. viverrini* transcriptomic data sets.				
Total reads with nucleotide mismatches[a]				
Adult Illumina (11,095,483 reads)		2,899,708 (26.1%)	2,807,518 (25.3%)	
Juvenile Illumina (20,927,408 reads)		5,886,209 (25.3%)	5,815,073 (28.1%)	
Adult 454 (606,603 reads) [b]		307,879 (50.8%	308,114 (50.8%)	

[a] Nucleotide matches refers to RNA-seq reads that mapped to the genome with more than one nucleotide difference across the aligned region.

[b] Only considering Roche 454 reads for which >= 200 bases were mapped across the query and reference sequences.

Supplementary Table 3. Completeness of the *Opisthorchis viverrini, Clonorchis sinensis*, *Schistosoma haematobium*, *S. japonicum* and *S. mansoni* genomes (Class Trematoda) based on the identification of 248 ultra-conserved core eukaryotic genes (CEGs) within assembled scaffolds and general statistics of their predicted protein-coding gene sets

Gene sets	Number of CEGs	Completeness[b]	Total genes predicted	Gene length[a]	Coding domain length[a]	Average coding domain GC ratio	Average exons per gene	Exon length (bases)[a]	Intron length (bases)[a]
Trematoda									
Opisthorchiidae									
Opisthorchis viverrini	121/214[c]	48.8/86.3	16,379	18,231 ± 22,071; 99-228,146	1,298 ± 1,559; 90-32,823	47.8%	5.8	254 ± 324; 3-13,713	3,531 ± 5786; 1-186,537
Clonorchis sinensis	122/213	49.2/85.9	13,634	17,797 ± 18,657; 150-196,431	1,589 ± 1,569; 150-48,060	48.0%	6.9	232 ± 324; 3-13,736	2,761 ± 3745; 2-68,640
Schistosomatidae									
Schistosoma haematobium	140/210	56.5/84.7	13,073	11,952 ± 16,273; 30–204,220	1,308 ± 1,498; 30 - 28,212	36.4%	5.4	246 ± 287; 1–9,737	2,442 ± 2,958; 1–68,754
Schistosoma japonicum	132/213	53.2/85.9	13,469	10,003 ± 12,980;150–173,394	1,179 ± 1,201; 147–24,180	36.2%	4.4	216 ± 244; 6–6,326	2,058 ± 2,679; 15–59,770
Schistosoma mansoni	136/198	54.8/79.8	13,191	12,509 ± 18,848; 3-233,688	1,340 ± 1,446; 60-22,980	36.9%	5.4	219 ± 267; 1-15,688	2,462 ± 3,545; 1-177,536

[a] Average nucleotide bases; Standard deviation; Minimum-maximum
[a] Percentage of 248 ultra-conserved CEGs present.
[b] Complete/partial matches.

Supplementary Table 4. Genome-wide comparisons of *Opisthorchis viverrini*, *Clonorchis sinensis* and *Schistosoma mansoni.*

Sequence datasets used to compare genome-wide similarity and synteny among parasitic flatworms.

	Sequences	Nucleotide bases (kb)
Clonorchis sinensis		
Top 10 scaffolds with amino acid homology to O. viverrini	10	7,347
Scaffolds with similarity to O. viverrini *scaffold Opera_V5_1*	63	17,467
Scaffolds with similarity to S. mansoni *chromosome 1 (> 100 kb)*	563	165,270
Opisthorchis viverrini		
Top 10 scaffolds with amino acid homology to C. sinensis	10	29,889
O. viverrini scaffold Oviv_Opera_V5_1	1	9,657
Scaffolds with similarity to S. mansoni *chromosome 1 (> 100 kb)*	308	386,773
Schistoma mansoni		
Chromosome 1	1	65,476

Genome-wide similarity

Nucleotide similarity	Aligned kilobases (Reference)	Aligned kilobases (Query)	Average length (Reference/Query)	Average Identity	Average Similarity
O. viverrini vs. *C. sinensis*[a]	139,828 (22.0%)	141,287 (25.8%)	749/753	85.0%	n/a
Amino acid similarity					
O. viverrini vs. *C. sinensis*[a]	240,299 (37.9%)	219,728 (40.2%)	326/327	71.5%	77.7%
S. mansoni vs. *O. viverrini*[a]	5,699 (1.6%)	9,351 (1.5%)	266/265	72.9%	81.5%
S. mansoni vs. *C. sinensis* [a]	5,569 (1.5%)	8,322 (1.5%)	178/178	73.8%	82.3%

Genome synteny of selected scaffolds

Syntenic Blocks	Coverage in aligned scaffolds [Reference/Query]	Number of syntenic blocks	Blocks less than 100 kb [Reference/Query]	Blocks more than 100 kb [Reference/Query]	Coverage of aligned scaffolds in syntenic blocks [Reference/Query]
Top 10 homologous scaffolds of *O. viverrini* and *C. sinensis*					
O. viverrini vs. *C. sinensis*[a]	14% / 56%	13	1 / 3	12 / 10	29% / 87%
Comparison between the largest *O. viverrini* scaffold and *C. sinensis* genome scaffolds greater than 100 kb.					
O. viverrini vs. *C. sinensis*[a]	54% / 33%	52	26 / 21	26 / 31	85% / 48%
Comparison between *S. mansoni* chromosome 1, and *O. viverrini* and *C. sinensis* genome scaffolds greater than 100 kb.					
S. mansoni vs. *O. viverrini*[a]	1% / < 0.1%	107	50 / 41	57 / 66	35% / 8%
S. mansoni vs. *C. sinensis* [a]	1% /< 0.1%	65	51 / 39	14 / 26	9% / 3%

[a]Reference vs. Query

Supplementary Table 5. Functions predicted for proteins encoded in the genome of *Opisthorchis viverrini* based on gene ontology (GO). The parental (= level 2) and level 5 GO categories were assigned according to InterPro domains with similarity to functionally annotated genes.

	Genes	Proportion of genes (%)	Top level 5 GO terms (number of genes)
Total number of protein-encoding genes with gene ontology annotation	6542		
GO:0008150 biological process	3985	60.8	
GO:0009987 cellular process	3060	46.7	GO:0044260 cellular macromolecule metabolic process (1596); GO:0034641 cellular nitrogen compound metabolic process (1178); GO:0044249 cellular biosynthetic process (997)
GO:0008152 metabolic process	2762	42.1	GO:0044260 cellular macromolecule metabolic process (1596); GO:0034641 cellular nitrogen compound metabolic process (1178); GO:0006139 nucleobase-containing compound metabolic process (1154)
GO:0065007 biological regulation	872	13.3	GO:0050794 regulation of cellular process (836); GO:0019222 regulation of metabolic process (348); GO:0023051 regulation of signaling (95)
GO:0050789 regulation of biological process	848	12.9	GO:0007165 signal transduction (508); GO:0080090 regulation of primary metabolic process (340); GO:0031323 regulation of cellular metabolic process (339)
GO:0051179 localization	673	10.3	GO:0006810 transport (663); GO:0008104 protein localization (170); GO:0045184 establishment of protein localization (161)
GO:0051234 establishment of localization	664	10.1	GO:0055085 transmembrane transport (255); GO:0006811 ion transport (236); GO:0015031 protein transport (161)
GO:0050896 response to stimulus	602	9.2	GO:0007165 signal transduction (508); GO:0009966 regulation of signal transduction (94); GO:0033554 cellular response to stress (61)
GO:0023052 signaling	513	7.8	GO:0035556 intracellular signal transduction (232); GO:0007166 cell surface receptor signaling pathway (153); GO:0009966 regulation of signal transduction (94)
GO:0071840 cellular component organization or biogenesis	218	3.3	GO:0071842 cellular component organization at cellular level (181); GO:0022607 cellular component assembly (111); GO:0043933 macromolecular complex subunit organization (111)
GO:0022610 biological adhesion	85	1.3	GO:0016337 cell-cell adhesion (53); GO:0031589 cell-substrate adhesion (2)
GO:0048519 negative regulation of biological process	36	0.6	GO:0010605 negative regulation of macromolecule metabolic process (13); GO:0031324 negative regulation of cellular metabolic process (13); GO:0010648 negative regulation of cell communication (12)
GO:0032502 developmental process	31	0.5	GO:0030154 cell differentiation (6); GO:0007548 sex differentiation (4); GO:0045596 negative regulation of cell differentiation (2)
GO:0032501 multicellular organismal process	27	0.4	GO:0050877 neurological system process (4); GO:0046660 female sex differentiation (1); GO:0019226 transmission of nerve impulse (1)
GO:0022414 reproductive process	18	0.3	GO:0003006 developmental process involved in reproduction (4); GO:0007548 sex differentiation (4)
GO:0000003 reproduction	18	0.3	GO:0022414 reproductive process (18); GO:0003006 developmental process involved in reproduction (4)
GO:0016265 death	10	0.2	GO:0012501 programmed cell death (10); GO:0010941 regulation of cell death (7)
GO:0048518 positive regulation of biological process	4	0.1	GO:0048522 positive regulation of cellular process (4); GO:0009893 positive regulation of metabolic process (4)
GO:0002376 immune system process	3	0.1	GO:0006955 immune response (3)
GO:0040007 growth	2	0.0	GO:0040008 regulation of growth (2); GO:0016049 cell growth (2)
GO:0005575 cellular component	2516	38.4	
GO:0005623 cell	1670	25.5	GO:0005622 intracellular (1572); GO:0071944 cell periphery (105); GO:0012505 endomembrane system (66)
GO:0016020 membrane	1068	16.3	GO:0031224 intrinsic to membrane (493); GO:0044459 plasma membrane part (43); GO:0042175 nuclear outer membrane-endoplasmic reticulum membrane network (32)
GO:0043226 organelle	836	12.8	GO:0043231 intracellular membrane-bounded organelle (528); GO:0044446 intracellular organelle part (381); GO:0043232 intracellular non-membrane-bounded organelle (361)
GO:0032991 macromolecular complex	568	8.7	GO:0005840 ribosome (107); GO:0005875 microtubule associated complex (76); GO:0005874 microtubule (54)
GO:0005576 extracellular region	56	0.9	GO:0005578 proteinaceous extracellular matrix (24); GO:0005615 extracellular space (2); GO:0044217 other organism part (1)
GO:0031974 membrane-enclosed lumen	56	0.9	GO:0043233 organelle lumen (52); GO:0031970 organelle envelope lumen (4)
GO:0031012 extracellular matrix	26	0.4	GO:0005581 collagen (9)
GO:0045202 synapse	22	0.3	GO:0097060 synaptic membrane (16); GO:0008021 synaptic vesicle (6)
GO:0030054 cell junction	20	0.3	GO:0005921 gap junction (16); GO:0043296 apical junction complex (1); GO:0070160 occluding junction (1)

GO:0003674 molecular function	5855	89.3	
GO:0005488 binding	4241	64.7	GO:0000166 nucleotide binding (1150); GO:0043169 cation binding (991); GO:0003677 DNA binding (425)
GO:0003824 catalytic activity	2620	40.0	GO:0016772 transferase activity, transferring phosphorus-containing groups (675); GO:0016817 hydrolase activity, acting on acid anhydrides (411); GO:0008233 peptidase activity (388)
GO:0005215 transporter activity	390	6.0	GO:0022891 substrate-specific transmembrane transporter activity (292); GO:0022803 passive transmembrane transporter activity (139); GO:0022804 active transmembrane transporter activity (122)
GO:0030234 enzyme regulator activity	184	2.8	GO:0030695 GTPase regulator activity (102); GO:0030414 peptidase inhibitor activity (49); GO:0061135 endopeptidase regulator activity (48)
GO:0005198 structural molecule activity	181	2.8	GO:0003735 structural constituent of ribosome (107); GO:0005201 extracellular matrix structural constituent (9); GO:0017056 structural constituent of nuclear pore (3)
GO:0001071 nucleic acid binding transcription factor activity	172	2.6	GO:0003700 sequence-specific DNA binding transcription factor activity (172)
GO:0060089 molecular transducer activity	115	1.8	GO:0038023 signaling receptor activity (77); GO:0005057 receptor signaling protein activity (11)
GO:0004872 receptor activity	95	1.5	GO:0004888 transmembrane signaling receptor activity (48); GO:0003707 steroid hormone receptor activity (23); GO:0030594 neurotransmitter receptor activity (8)
GO:0009055 electron carrier activity	30	0.5	GO:0009055 electron carrier activity (30)
GO:0000988 protein binding transcription factor activity	20	0.3	GO:0003712 transcription cofactor activity (20); GO:0001076 RNA polymerase II transcription factor binding transcription factor activity (15)
GO:0016209 antioxidant activity	14	0.2	GO:0004784 superoxide dismutase activity (5) ;GO:0004601 peroxidase activity (2); GO:0004791 thioredoxin-disulfide reductase activity (1)

Supplementary Table 6. Classification of *Opisthorchis viverrini*, *Schistosoma haematobium* and *Taenia solium* genes based on conceptually translated amin acid sequence homology (BLASTp, $< 10^{-05}$) to KEGG orthologues genes and conservation within parasite specific taxonomic families to the exclusion of the other parasitic flatworm families that were included in this study based on OrthoMCL clustering.

	Opisthorchis viverrini		Opisthorchiidae[b] (OrthoMCL groups)			*Schistosoma haematobium*		Schistosomatidae[c] (OrthoMCL groups)		*Taenia solium*		Taeniidae[d] (OrthoMCL)	
	K terms[a]	Genes	K terms	Genes	% of total genes	K terms	Genes	K terms	Genes	K terms	Genes	K terms	Genes
KEGG protein classes													
Cellular Processes													
Cell Motility													
Cytoskeleton proteins	72	213	14	37	17.4	69	169	12	20	75	221	23	55
Environmental Information Processing													
Membrane Transport													
Solute carrier family	106	202	19	24	11.9	100	216	23	30	95	174	22	33
Transporters	40	74	8	11	14.9	32	59	7	8	28	56	5	5
Secretion system	10	13	1	1	7.7	12	13	7	7	15	15		
Signaling Molecules and Interaction													
Nuclear receptors	14	22	10	10	45.5	17	21	5	5	12	13	7	7
Ion channels	62	128	13	18	14.1	62	111	10	10	68	170	20	30
G protein-coupled receptors	33	59	7	13	22.0	29	63	9	11	25	49	8	10
GTP-binding proteins	57	87	6	7	8.0	56	76	8	16	52	73	11	12
Cellular antigens	40	74	8	9	12.2	32	65	6	9	33	89	12	19
Cell adhesion molecules (CAMs)	22	34	4	4	11.8	20	35	3	3	21	30	2	2
CAM ligands	16	31	4	5	16.1	15	32	3	4	16	42	6	10
Cytokine receptors	24	31	6	6	19.4	15	27	2	2	17	25	4	4
Enzyme-linked receptors	23	30	6	6	20.0	14	26	2	2	16	24	4	4
Glycan bindng proteins	9	12	1	1	8.3	9	14	3	4	10	13	1	1
Genetic Information Processing													
Folding, Sorting and Degradation													
Ubiquitin system	228	282	27	30	10.6	225	298	36	61	220	340	39	47
Chaperones and folding catalysts	95	130	6	8	6.2	95	128	18	27	88	192	10	12
Proteasome	46	59	1	2	3.4	50	56	13	14	50	125	3	4
SNAREs	17	25				18	23	3	4	18	22	2	2
Replication and Repair													
Chromosome	207	334	23	23	6.9	204	335	45	71	213	358	45	50
DNA repair and recombination proteins	140	169	9	9	5.3	138	183	39	49	139	180	16	17
DNA replication proteins	82	106	3	3	2.8	81	110	23	28	80	123	8	11
Translation													
Ribosome biogenesis	149	191	6	7	3.7	157	214	42	64	147	242	6	8
Transfer RNA biogenesis	101	140	4	4	2.9	104	150	32	46	99	142	8	8
Ribosome	69	77				70	84	24	29	78	85		

Translation factors	50	65				51	65	18	22	50	59		
Transcription													
Transcription factors	155	226	93	120	53.1	166	226	82	92	166	252	106	130
Spliceosome	210	328	16	22	6.7	209	293	40	70	216	350	30	37
Transcription machinery	134	186	10	14	7.5	136	181	26	40	137	192	19	23
Metabolism													
Amino Acid Metabolism													
Amino acid related enzymes	29	47	2	2	4.3	28	54	19	26	30	46	1	1
Enzyme Families													
Peptidases	143	343	20	43	12.5	141	216	22	31	131	201	12	14
Protein kinases	169	265	22	27	10.2	159	281	33	48	163	291	36	45
Glycan Biosynthesis and Metabolism													
Glycosyltransferases	46	85	8	18	21.2	47	77	11	11	50	87	8	13
Proteoglycans	8	8	1	1	12.5	10	10	2	2	8	10	3	3
Lipid Metabolism													
Lipid biosynthesis proteins	25	40	2	3	7.5	23	36	4	5	22	35	3	5

[a] K terms represent sequence homology to specific KEGG orthologues gene groups/terms within the KEGG database

[b] Opisthorchiidase includes gene sets from *Clonorchis sinensis and Opisthorchis viverrini*

[c] Schistosomatida includes gene sets from *Schistosoma haematobium, S. japonicum and S. mansoni*

[d] Taeniidae includes gene sets from *Echinococcus granulosis, E. multilocularis and Taenia solium*

Supplementary Table 7. Predicted *Opisthorchis viverrini* proteins with orthologues in *Clonorchis sinensis* and which diverged in amino acid sequence simialrity when compared to other trematode (*S. haematobium*, *S. japonicum* and *S. mansoni*) and cestodes (*Echinococcus granulosus*, *E. multilocularis* and *Taenia solium*) using OrthoMCL clustering.

Protein family	Number of genes	Top KEGG protein family genes[a]
Genetic Information Processing; Transcription	119	KRAB domain-containing zinc finger protein (9); GATA-binding protein 1/2/3 (4); SOX1S; transcription factor SOX1/2/3/14/21 (SOX group B) (4)
Metabolism; Peptidases	43	Cathepsin D (11); Pepsin A (5); Leishmanolysin-like peptidase (4)
Cellular Processes; Cell Motility; Cytoskeleton proteins	37	Dyneins (23); Kinesins (6); Tubulins (2)
Genetic Information Processing;Folding, Sorting and Degradation; Ubiquitin system	29	Ubiquitin ligases (E3) multi subunit Ring-finger type E3 Cul3 complex target recognizing subunit (BTB) (6); Ubiquitin ligases (E3) multi subunit Ring-finger type E3 SCF complex target recognizing subunit (F-box) (4); Ubiquitins and Ubiquitin-like proteins Ubiquitin-like
Environmental Information Processing; Membrane Transport; Solute carrier family	23	Na+-independent, system-L-like amino acid transporter (3); Cationic amino acid transporter (2); Na+/H+ exchanger SLC9A3, NHE3 (2)
Environmental Information Processing; Signaling Molecules and Interaction; Ion channels	18	Transient receptor potential cation channel subfamily A member 1 (4); Glycine receptor alpha-3 (2); Glycerol uptake receptor (2)
Metabolism; Glycan Biosynthesis and Metabolism; Glycosyltransferases	14	Glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase (4); N-acetyllactosaminide beta-1,6-N-acetylglucosaminyl-transferase (2); alpha-1,6-mannosyl-glycoprotein 6-beta-N-acetylglucosaminyltransferase (2)
Environmental Information Processing; Signaling Molecules and Interaction; G protein-coupled receptors	13	Dopamine D2-like receptor (2); 5-hydroxytryptamine receptor 1 (2)
Environmental Information Processing; Membrane Transport;Transporters	11	MFS transporter, LAT3 family, solute carrier family 43, member 3 (3); MFS transporter, OCT family, solute carrier family 22 (organic cation transporter), member 4/5 (2); ATP-binding cassette, subfamily A (ABC1), member 5 (1)
Environmental Information Processing; Signaling Molecules and Interaction; Nuclear receptors	10	Thyroid hormone like (4); Hepatocyte nuclear factor 4 like (5); Nerve growth factor IB like (1)

[a]The three most frequently reported KEGG protein families within each protein family group are reported

Supplementary Table 8. Classified *Opisthorchis viverrini* G-coupled protein receptors (GPCRs). The level of transcription of each gene in juvenle and adult stages is shown as reads per kilobase per million reads (RPKM).

Gene	Adult RPKM	Juvenile RPKM	Level of transcription	Swissprot match	E-value	KEGG term	KEGG orthologous gene term description	KEGG protein classification	E-value
T265_08227	16.17	26.38	MEDIUM	sp#P20905#5HT1R_DROME 5-hydroxytryptamine receptor 1 OS=Drosophila melanogaster GN=5-HT7 PE=2 SV=1	1.00E-49	K04163	smm:Smp_148210 biogenic amine (5HT) receptor	Receptor|Class A. Rhodopsin family|Biogenic amine [Fig]|Serotonin [Table]| HTR7; 5-hydroxytryptamine receptor 7	5.00E-70
T265_08477	12.22	27.03	MEDIUM	sp#Q8BKG4#FZD10_MOUSE Frizzled-10 OS=Mus musculus GN=Fzd10 PE=2 SV=1	4.00E-90	K02842	smm:Smp_174350 frizzled-like receptor ; K02842 frizzled 9/10	Receptor|Others|Wnt signaling|Frizzled / Smoothened family| FZD9_10; frizzled 9/10	5.00E-168
T265_08023	16.78	19.43	MEDIUM	sp#Q14831#GRM7_HUMAN Metabotropic glutamate receptor 7 OS=Homo sapiens GN=GRM7 PE=1 SV=1	3.00E-64	K04611	smm:Smp_128940 metabotropic glutamate receptor ; K04611 metabotropic X receptor	Receptor|Class C. Metabotropic glutamate receptor family|Biogenic amine|Glutamate (metabotropic) [Table]| MXR; metabotropic X receptor	1.00E-149
T265_10062	10.21	20.99	MEDIUM	sp#Q98998#5HT1A_XENLA 5-hydroxytryptamine receptor 1A OS=Xenopus laevis GN=htr1a PE=2 SV=1	1.00E-63	K04163	smm:Smp_126730 biogenic amine (5HT) receptor ; K04163 5-hydroxytryptamine receptor 7	Receptor|Class A. Rhodopsin family|Biogenic amine [Fig]|Serotonin [Table]| HTR7; 5-hydroxytryptamine receptor 7	2.00E-122
T265_14297	19.69	8.55	MEDIUM	sp#Q9NYQ6#CELR1_HUMAN Cadherin EGF LAG seven-pass G-type receptor 1 OS=Homo sapiens GN=CELSR1 PE=1 SV=1	5.00E-07	K04600	smm:Smp_165970 acidic fibroblast growth factor intracellular binding protein	Receptor|Class B. Secretin receptor family|Cell adhesion|Cadherin EGF LAG (CELSR)| CELSR1; cadherin EGF LAG seven-pass G-type receptor 1 (flamingo)	3.00E-13
T265_05670	12.15	12.91	MEDIUM	sp#Q9I9M5#FZD1_XENLA Frizzled-1 OS=Xenopus laevis GN=fzd1 PE=2 SV=1	1.00E-91	K02432	smm:Smp_118970 frizzled-like receptor ; K02432 frizzled 1/7	Receptor|Others|Wnt signaling|Frizzled / Smoothened family| FZD1_7, fz; frizzled 1/7	4.00E-134
T265_16020	8.46	10.61	MEDIUM	sp#Q9I9M5#FZD1_XENLA Frizzled-1 OS=Xenopus laevis GN=fzd1 PE=2 SV=1	2.00E-58	K02432	smm:Smp_173940 frizzled	Receptor|Others|Wnt signaling|Frizzled / Smoothened family| FZD1_7, fz; frizzled 1/7	1.00E-106
T265_10860	9.68	8.21	MEDIUM	sp#O42224#SMO_CHICK Smoothened homolog (Fragment) OS=Gallus gallus GN=SMO PE=2 SV=1	5.00E-10	K06226	smm:Smp_125160 hypothetical protein	Receptor|Others|Wnt signaling|Frizzled / Smoothened family| SMO; smoothened	5.00E-57
T265_14420	8.66	9.06	MEDIUM	sp#Q9NYQ6#CELR1_HUMAN Cadherin EGF LAG seven-pass G-type receptor 1 OS=Homo sapiens GN=CELSR1 PE=1 SV=1	3.00E-12	K08446	smm:Smp_153600 hypothetical protein	CD|CD (clusters of differentiation) molecules| CD97; CD97 antigen [HSA:976]	0.00E+00
T265_09923	10.93	6.32	MEDIUM	sp#O93274#FZD8_XENLA Frizzled-8 OS=Xenopus laevis GN=fzd8 PE=2 SV=1	7.00E-125	K02375	smm:Smp_139180 frizzled-like receptor ; K02375 frizzled 5/8	Receptor|Others|Wnt signaling|Frizzled / Smoothened family| FZD5_8, fz2; frizzled 5/8	2.00E-179
T265_08251	5.62	6.98	MEDIUM	sp#Q8IS44#DRD2L_DROME Dopamine D2-like receptor OS=Drosophila melanogaster GN=D2R PE=2 SV=1	3.00E-28	K14049	smm:Smp_127310 biogenic amine (dopamine) receptor ; K14049 dopamine D2-like receptor	Receptor|Class A. Rhodopsin family|Biogenic amine [Fig]|Dopamine [Table]| DRD2N; dopamine D2-like receptor	8.00E-42
T265_14576	5.4	6.76	MEDIUM	sp#P30975#TLR2_DROME Tachykinin-like peptides receptor 99D OS=Drosophila melanogaster GN=Takr99D PE=2 SV=2	3.00E-50	K04225	dpe:Dper_GL13493 GL13493 gene product from transcript GL13493-RA; K04225 tachykinin-like receptor	Receptor|Class A. Rhodopsin family|Neuropeptide|Tachykinin [Table]| TAKR; tachykinin-like receptor	7.00E-51
T265_14587	5.17	6.1	MEDIUM	sp#P24628#DRD2A_XENLA D(2) dopamine receptor A OS=Xenopus laevis GN=drd2-a PE=2 SV=1	2.00E-31	K04145	nvi:100120086 NV_30025, NV50024; putative tyramine/octopamine receptor	Receptor|Class A. Rhodopsin family|Biogenic amine [Fig]|Dopamine [Table]| DRD2; dopamine receptor D2	3.00E-32
T265_02641	2.91	7.56	MEDIUM	sp#Q9PWH2#FZD10_CHICK Frizzled-10 OS=Gallus gallus GN=FZD10 PE=2 SV=1	2.00E-50	K02354	phu:Phum_PHUM440660 class D atypical G-protein coupled receptor GPRfz3, putative; K02354 frizzled 4	Receptor|Others|Wnt signaling|Frizzled / Smoothened family| FZD4, fz4; frizzled 4	3.00E-62
T265_00683	3.58	6.18	MEDIUM	sp#Q6VMN6#PRLHR_MOUSE Prolactin-releasing peptide receptor OS=Mus musculus GN=Prlhr PE=2 SV=2	4.00E-41	K04209	smm:Smp_118040 neuropeptide receptor ; K04209 neuropeptide Y receptor, invertebrate	Receptor|Class A. Rhodopsin family|Neuropeptide|Neuropeptide Y [Table]| NPYNR; neuropeptide Y receptor, invertebrate	4.00E-124
T265_00777	2.51	6.79	MEDIUM	sp#Q868T3#CCAPR_DROME Cardioacceleratory peptide receptor OS=Drosophila melanogaster GN=CcapR PE=2 SV=3	2.00E-34	K08376	smm:Smp_126890 G-protein coupled receptor fragment	Receptor|Class A. Rhodopsin family|Neuropeptide|Neuropeptide S| NPSR1, GPR154; neuropeptide S receptor 1	9.00E-62
T265_14490	6.08	3.17	MEDIUM	sp#Q9CSB4#PAR3L_MOUSE Partitioning defective 3 homolog B OS=Mus musculus GN=Pard3b PE=1 SV=2	2.00E-11	K04237	smm:Smp_127800 sap-97	Receptor|Class A. Rhodopsin family|Complement peptide|Thrombin| PARD3; partitioning defective protein 3	2.00E-27
T265_12797	2.38	6.62	MEDIUM	sp#Q9VEU1#CAD89_DROME Cadherin-89D OS=Drosophila melanogaster GN=Cad89D PE=2 SV=3	1.00E-09	K04601	smm:Smp_162550 cadherin	Receptor|Class B. Secretin receptor family|Cell adhesion|Cadherin EGF LAG (CELSR)| CELSR2; cadherin EGF LAG seven-pass G-type receptor 2 (flamingo)	1.00E-72
T265_06492	2.8	4.5	MEDIUM	sp#Q8WPA2#AR_BOMMO Allatostatin-A receptor OS=Bombyx mori GN=AR PE=2 SV=1	2.00E-44	K04233	smm:Smp_011940 peptide (allatostatin)-like receptor ; K04233 allatostatin receptor	Receptor|Class A. Rhodopsin family|Neuropeptide|Galanin [Table]| GALRN, AR; allatostatin receptor	2.00E-86
T265_06423	2.04	4.97	MEDIUM	sp#P34992#NPY1R_XENLA Neuropeptide Y receptor type 1 OS=Xenopus laevis GN=npy1r PE=2 SV=1	5.00E-15	K04204	smm:Smp_133550 neuropeptide F-like receptor	Receptor|Class A. Rhodopsin family|Neuropeptide|Neuropeptide Y [Table]| NPY1R_4R_6R; neuropeptide Y receptor type 1/4/6	6.00E-79
T265_02775	2.28	4.63	MEDIUM	sp#Q09388#ACM2_CAEEL Probable muscarinic acetylcholine receptor gar-2 OS=Caenorhabditis elegans GN=gar-2 PE=2 SV=3	1.00E-46	K04134	smm:Smp_145540 muscarinic acetylcholine (GAR) receptor ; K04134 muscarinic acetylcholine receptor	Receptor|Class A. Rhodopsin family|Biogenic amine [Fig]|Acetylcholine (muscarinic) [Table]| CHRMN; muscarinic acetylcholine receptor	1.00E-109
T265_13022	2.34	4.36	MEDIUM	sp#Q24292#DS_DROME Protein dachsous OS=Drosophila melanogaster GN=ds PE=1 SV=3	3.00E-29	K04601	smm:Smp_167460 cadherin	Receptor|Class B. Secretin receptor family|Cell adhesion|Cadherin EGF LAG (CELSR)| CELSR2; cadherin EGF LAG seven-pass G-type receptor 2 (flamingo)	0.00E+00
T265_13740	2.76	3.84	MEDIUM	sp#Q9V5N8#STAN_DROME Protocadherin-like wing polarity protein stan OS=Drosophila melanogaster GN=stan PE=1 SV=4	6.00E-11	K04600	ame:551848 protocadherin-like wing polarity protein stan-like; K04600 cadherin EGF LAG seven-pass G-type receptor 1 (flamingo)	Receptor|Class B. Secretin receptor family|Cell adhesion|Cadherin EGF LAG (CELSR)| CELSR1; cadherin EGF LAG seven-pass G-type receptor 1 (flamingo)	4.00E-12
T265_08353	1.45	4.86	MEDIUM	sp#Q8IS44#DRD2L_DROME Dopamine D2-like receptor OS=Drosophila melanogaster GN=D2R PE=2 SV=1	1.00E-24	K14049	smm:Smp_127720 G-protein coupled receptor fragment	Receptor|Class A. Rhodopsin family|Biogenic amine [Fig]|Dopamine [Table]| DRD2N; dopamine D2-like receptor	1.00E-42
T265_02329	0.73	4.73	MEDIUM	sp#Q18775#DOPR4_CAEEL Dopamine receptor 4 OS=Caenorhabditis elegans GN=dop-4 PE=2 SV=2	2.00E-27	K04157	ame:411323 5-HT2alpha; serotonin receptor; K04157 5-hydroxytryptamine receptor 2	Receptor|Class A. Rhodopsin family|Biogenic amine [Fig]|Serotonin [Table]| HTR2; 5-hydroxytryptamine receptor 2	3.00E-28
T265_13579	4.12	1.34	MEDIUM	sp#O93274#FZD8_XENLA Frizzled-8 OS=Xenopus laevis GN=fzd8 PE=2 SV=1	2.00E-116	K02375	smm:Smp_155340 frizzled-like receptor	Receptor|Others|Wnt signaling|Frizzled / Smoothened family| FZD5_8, fz2; frizzled 5/8	8.00E-151
T265_03837	1.96	3.24	MEDIUM	sp#P56719#OX2R_RAT Orexin receptor type 2 OS=Rattus norvegicus GN=Hcrtr2 PE=2 SV=1	2.00E-11	K04239	smm:Smp_140620 G-protein coupled receptor fragment	Receptor|Class A. Rhodopsin family|Neuropeptide|Orexin| HCRTR2; hypocretin (orexin) receptor 2	2.00E-14
T265_08249	2.95	2.24	MEDIUM	sp#Q8IS44#DRD2L_DROME Dopamine D2-like receptor OS=Drosophila melanogaster GN=D2R PE=2 SV=1	1.00E-15	K14049	smm:Smp_127310 biogenic amine (dopamine) receptor ; K14049 dopamine D2-like receptor	Receptor|Class A. Rhodopsin family|Biogenic amine [Fig]|Dopamine [Table]| DRD2N; dopamine D2-like receptor	9.00E-23
T265_03164	2.94	1.83	MEDIUM	sp#Q9WU25#ADA1A_CAVPO Alpha-1A adrenergic receptor OS=Cavia porcellus GN=ADRA1A PE=2 SV=2	3.00E-07	K04135	smm:Smp_083880 G-protein coupled receptor fragment	Receptor|Class A. Rhodopsin family|Biogenic amine [Fig]|Adrenaline [Table]| ADRA1A; adrenergic receptor alpha-1A	6.00E-26
T265_15194	1.69	2.74	MEDIUM	sp#Q09388#ACM2_CAEEL Probable muscarinic acetylcholine receptor gar-2 OS=Caenorhabditis elegans GN=gar-2 PE=2 SV=3	2.00E-24	K04134	smm:Smp_152540 G-protein coupled receptor fragment	Receptor|Class A. Rhodopsin family|Biogenic amine [Fig]|Acetylcholine (muscarinic) [Table]| CHRMN; muscarinic acetylcholine receptor	8.00E-37
T265_08405	1.23	3.18	MEDIUM	sp#Q9VNM1#NPFR1_DROME Neuropeptide F receptor OS=Drosophila melanogaster GN=NPFR1 PE=1 SV=3	3.00E-21	K04209	smm:Smp_133550 neuropeptide F-like receptor	Receptor|Class A. Rhodopsin family|Neuropeptide|Neuropeptide Y [Table]| NPYNR; neuropeptide Y receptor, invertebrate	3.00E-37

T265_08621	2.46	1.92	MEDIUM	sp#Q9N298#5HT1A_PANTR 5-hydroxytryptamine receptor 1A OS=Pan troglodytes GN=HTR1A PE=3 SV=1	3.00E-36	K04163	smm:Smp_126730 biogenic amine (5HT) receptor ; K04163 5-hydroxytryptamine receptor 7	Receptor|Class A. Rhodopsin family|Biogenic amine [Fig]|Serotonin [Table]| HTR7; 5-hydroxytryptamine receptor 7	3.00E-48
T265_04058	1.77	2.54	MEDIUM	sp#Q25414#5HTR_LYMST 5-hydroxytryptamine receptor OS=Lymnaea stagnalis PE=2 SV=1	7.00E-44	K04153	smm:Smp_149770 G-protein coupled receptor fragment	Receptor|Class A. Rhodopsin family|Biogenic amine [Fig]|Serotonin [Table]| HTR1; 5-hydroxytryptamine receptor 1	3.00E-49
T265_14776	1.63	2.19	MEDIUM	sp#Q9V5N8#STAN_DROME Protocadherin-like wing polarity protein stan OS=Drosophila melanogaster GN=stan PE=1 SV=4	1.00E-08	K04600	smm:Smp_055240 cadherin	Receptor|Class B. Secretin receptor family|Cell adhesion|Cadherin EGF LAG (CELSR)| CELSR1; cadherin EGF LAG seven-pass G-type receptor 1 (flamingo)	2.00E-15
T265_09554	1.07	2.68	MEDIUM	sp#P25931#NPYR_DROME Neuropeptide Y receptor OS=Drosophila melanogaster GN=NepYr PE=2 SV=2	1.00E-41	K14072	smm:Smp_058080 G-protein coupled receptor fragment	Receptor|Class A. Rhodopsin family|Neuropeptide|Tachykinin [Table]| NEPYR; neuropeptide Y receptor	1.00E-79
T265_15635	1.15	1.5	LOW			K04585		Receptor|Class B. Secretin receptor family|Calcium-regulating peptide|Parathyroid hormone| PTHR1; parathyroid hormone receptor 1	
T265_09662	0.52	2.02	MEDIUM	sp#Q93126#GPR9_BALAM Probable G-protein coupled receptor No9 OS=Balanus amphitrite PE=3 SV=1	3.00E-49	K04165	ame:406068 Oa1, Oar; octopamine receptor; K04165 Octopamine receptor	Receptor|Class A. Rhodopsin family|Biogenic amine [Fig]|Octopamine| Oamb; Octopamine receptor	3.00E-54
T265_01604	0.93	1.57	LOW	sp#O08786#CCKAR_MOUSE Cholecystokinin receptor type A OS=Mus musculus GN=Cckar PE=2 SV=1	2.00E-07	K04196	smm:Smp_172810 rhodopsin-like orphan GPCR	Receptor|Class A. Rhodopsin family|Gut peptide|Cholecystokinin| CCKLR; cholecystokinin-like receptor	2.00E-86
T265_13638	1.77	0.38	LOW	sp#P09241#OPSD_ENTDO Rhodopsin OS=Enteroctopus dofleini GN=RHO PE=1 SV=1	1.00E-32	K04255	smm:Smp_180030 opsin-like receptor ; K04255 r-opsin	Receptor|Class A. Rhodopsin family|Vision|Opsin [Table]| OPN4, Rh2_7; r-opsin	5.00E-31
T265_01811	0.77	1.28	LOW	sp#Q25414#5HTR_LYMST 5-hydroxytryptamine receptor OS=Lymnaea stagnalis PE=2 SV=1	1.00E-26	K04153	api:100159225 5-hydroxytryptamine receptor-like; K04153 5-hydroxytryptamine receptor 1	Receptor|Class A. Rhodopsin family|Biogenic amine [Fig]|Serotonin [Table]| HTR1; 5-hydroxytryptamine receptor 1	6.00E-29
T265_12593	0.3	1.56	LOW	sp#P09241#OPSD_ENTDO Rhodopsin OS=Enteroctopus dofleini GN=RHO PE=1 SV=1	5.00E-43	K04255	smm:Smp_180030 opsin-like receptor ; K04255 r-opsin	Receptor|Class A. Rhodopsin family|Vision|Opsin [Table]| OPN4, Rh2_7; r-opsin	3.00E-40
T265_01409	0.76	1.09	LOW	sp#O01670#OAR2_LYMST Octopamine receptor 2 OS=Lymnaea stagnalis PE=1 SV=1	5.00E-61	K04153	smm:Smp_134820 biogenic amine (octopamine/dopamine) receptor ; K04153 5-hydroxytryptamine receptor 1	Receptor|Class A. Rhodopsin family|Biogenic amine [Fig]|Serotonin [Table]| HTR1; 5-hydroxytryptamine receptor 1	1.00E-55
T265_01234	0.13	1.67	LOW	sp#Q8WPA2#AR_BOMMO Allatostatin-A receptor OS=Bombyx mori GN=AR PE=2 SV=1	7.00E-10	K08374	smm:Smp_191150 hypothetical protein	Receptor|Class A. Rhodopsin family|Hypothalamic hormone|Kisspeptin| KISS1R; KISS1 receptor	3.00E-21
T265_00799	0.68	0.88	LOW	sp#Q17232#OAR_BOMMO Octopamine receptor OS=Bombyx mori PE=2 SV=1	3.00E-46	K04153	api:100163581 octopamine receptor beta-2R-like	Receptor|Class A. Rhodopsin family|Biogenic amine [Fig]|Serotonin [Table]| HTR1; 5-hydroxytryptamine receptor 1	4.00E-48
T265_12603	1.17	0.35	LOW	sp#Q9VNM1#NPFR1_DROME Neuropeptide F receptor OS=Drosophila melanogaster GN=NPFR1 PE=1 SV=3	2.00E-24	K04209	smm:Smp_126010 neuropeptide receptor	Receptor|Class A. Rhodopsin family|Neuropeptide|Neuropeptide Y [Table]| NPYNR; neuropeptide Y receptor, invertebrate	2.00E-28
T265_04998	0.21	1.24	LOW	sp#Q14832#GRM3_HUMAN Metabotropic glutamate receptor 3 OS=Homo sapiens GN=GRM3 PE=1 SV=2	2.00E-86	K04605	smm:Smp_052660 metabotropic glutamate receptor	Receptor|Class C. Metabotropic glutamate receptor family|Biogenic amine|Glutamate (metabotropic) [Table]| GRM2_3; metabotropic glutamate receptor 2/3	4.00E-169
T265_15636	0.6	0.63	LOW	sp#P23811#SCTR_RAT Secretin receptor OS=Rattus norvegicus GN=Sctr PE=2 SV=1	3.00E-09	K04585		Receptor|Class B. Secretin receptor family|Calcium-regulating peptide|Parathyroid hormone| PTHR1; parathyroid hormone receptor 1	
T265_13658	0	1.02	LOW	sp#P91685#GRM_DROME Metabotropic glutamate receptor OS=Drosophila melanogaster GN=mGluRA PE=1 SV=2	3.00E-88	K04605	smm:Smp_150370 metabotropic glutamate receptor 2 3 (mglur group 2)	Receptor|Class C. Metabotropic glutamate receptor family|Biogenic amine|Glutamate (metabotropic) [Table]| GRM2_3; metabotropic glutamate receptor 2/3	2.00E-150
T265_02545	0.44	0.46	LOW	sp#Q9DDN6#NPY2R_CHICK Neuropeptide Y receptor type 2 OS=Gallus gallus GN=NPY2R PE=3 SV=1	1.00E-43	K04209	smm:Smp_118040 neuropeptide receptor ; K04209 neuropeptide Y receptor, invertebrate	Receptor|Class A. Rhodopsin family|Neuropeptide|Neuropeptide Y [Table]| NPYNR; neuropeptide Y receptor, invertebrate	2.00E-76
T265_04385	0.13	0.72	LOW	sp#P25931#NPYR_DROME Neuropeptide Y receptor OS=Drosophila melanogaster GN=NepYr PE=2 SV=2	3.00E-18	K14072	smm:Smp_170020 neuropeptide receptor	Receptor|Class A. Rhodopsin family|Neuropeptide|Tachykinin [Table]| NEPYR; neuropeptide Y receptor	2.00E-46
T265_08199	0.27	0.42	LOW			K04149	bfo:BRAFLDRAFT_226966 hypothetical protein; K04149 histamine receptor H1	Receptor|Class A. Rhodopsin family|Biogenic amine [Fig]|Histamine [Table]| HRH1; histamine receptor H1	1.00E-05
T265_10363	0.44	0	LOW	sp#P25931#NPYR_DROME Neuropeptide Y receptor OS=Drosophila melanogaster GN=NepYr PE=2 SV=2	8.00E-27	K14072	smm:Smp_172170 G-protein coupled receptor fragment	Receptor|Class A. Rhodopsin family|Neuropeptide|Tachykinin [Table]| NEPYR; neuropeptide Y receptor	3.00E-51
T265_04947	0.39	0	LOW	sp#P09241#OPSD_ENTDO Rhodopsin OS=Enteroctopus dofleini GN=RHO PE=1 SV=1	6.00E-33	K04255	smm:Smp_180030 opsin-like receptor ; K04255 r-opsin	Receptor|Class A. Rhodopsin family|Vision|Opsin [Table]| OPN4, Rh2_7; r-opsin	2.00E-38
T265_02059	0.19	0.1	LOW			K04010	smm:Smp_001070.1 G-protein coupled receptor fragment	CD|CD (clusters of differentiation) molecules| CD88; complement component 5 receptor 1 [HSA:728]	3.00E-43
T265_05432	0.16	0.13	LOW	sp#P16423#POLR_DROME Retrovirus-related Pol polyprotein from type-2 retrotransposable element R2DM OS=Drosophila melanogaster GN=pol PE=4 SV=1	3.00E-13	K04209	smm:Smp_007070 G-protein coupled receptor fragment	Receptor|Class A. Rhodopsin family|Neuropeptide|Neuropeptide Y [Table]| NPYNR; neuropeptide Y receptor, invertebrate	4.00E-31
T265_01572	0	0.14	LOW	sp#Q8ITC7#CAPAR_DROME Neuropeptides capa receptor OS=Drosophila melanogaster GN=capaR PE=2 SV=3	9.00E-11	K05052	smm:Smp_141880 neuropeptide receptor	Receptor|Class A. Rhodopsin family|Neuropeptide|Neuromedin U| NMUR1; neuromedin U receptor 1	1.00E-16
T265_04946	0.13	0	LOW	sp#P09241#OPSD_ENTDO Rhodopsin OS=Enteroctopus dofleini GN=RHO PE=1 SV=1	6.00E-83	K04255	smm:Smp_104210 opsin-like receptor ; K04255 r-opsin	Receptor|Class A. Rhodopsin family|Vision|Opsin [Table]| OPN4, Rh2_7; r-opsin	5.00E-99